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**Genetic Stock Identification of Chinook Salmon
Harvest on the Yukon River 2009**

by

Nick A. DeCovich

and

Katherine G. Howard

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Alaska Department of Fish and Game

Divisions of Sport Fish and Commercial Fisheries



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Weights and measures (metric)		General		Mathematics, statistics	
centimeter	cm	Alaska Administrative Code	AAC	<i>all standard mathematical signs, symbols and abbreviations</i>	
deciliter	dL	all commonly accepted abbreviations	e.g., Mr., Mrs., AM, PM, etc.	alternate hypothesis	H_A
gram	g	all commonly accepted professional titles	e.g., Dr., Ph.D., R.N., etc.	base of natural logarithm	e
hectare	ha	at	@	catch per unit effort	CPUE
kilogram	kg	compass directions:		coefficient of variation	CV
kilometer	km	east	E	common test statistics	(F, t, χ^2 , etc.)
liter	L	north	N	confidence interval	CI
meter	m	south	S	correlation coefficient (multiple)	R
milliliter	mL	west	W	correlation coefficient (simple)	r
millimeter	mm	copyright	©	covariance	cov
		corporate suffixes:		degree (angular)	$^\circ$
Weights and measures (English)		Company	Co.	degrees of freedom	df
cubic feet per second	ft ³ /s	Corporation	Corp.	expected value	E
foot	ft	Incorporated	Inc.	greater than	>
gallon	gal	Limited	Ltd.	greater than or equal to	\geq
inch	in	District of Columbia	D.C.	harvest per unit effort	HPUE
mile	mi	et alii (and others)	et al.	less than	<
nautical mile	nmi	et cetera (and so forth)	etc.	less than or equal to	\leq
ounce	oz	exempli gratia	e.g.	logarithm (natural)	ln
pound	lb	(for example)		logarithm (base 10)	log
quart	qt	Federal Information Code	FIC	logarithm (specify base)	log ₂ , etc.
yard	yd	id est (that is)	i.e.	minute (angular)	'
		latitude or longitude	lat. or long.	not significant	NS
Time and temperature		monetary symbols (U.S.)	\$, ¢	null hypothesis	H_0
day	d	months (tables and figures): first three letters	Jan,...,Dec	percent	%
degrees Celsius	°C	registered trademark	®	probability	P
degrees Fahrenheit	°F	trademark	™	probability of a type I error (rejection of the null hypothesis when true)	α
degrees kelvin	K	United States (adjective)	U.S.	probability of a type II error (acceptance of the null hypothesis when false)	β
hour	h	United States of America (noun)	USA	second (angular)	"
minute	min	U.S.C.	United States Code	standard deviation	SD
second	s	U.S. state	use two-letter abbreviations (e.g., AK, WA)	standard error	SE
				variance	
Physics and chemistry				population	Var
all atomic symbols				sample	var
alternating current	AC				
ampere	A				
calorie	cal				
direct current	DC				
hertz	Hz				
horsepower	hp				
hydrogen ion activity (negative log of)	pH				
parts per million	ppm				
parts per thousand	ppt, ‰				
volts	V				
watts	W				

FISHERY DATA SERIES NO. 10-58

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HARVEST ON THE YUKON RIVER 2009**

by

Nick A. DeCovich and Katherine G. Howard

Alaska Department of Fish and Game, Division of Commercial Fisheries, Anchorage

Alaska Department of Fish and Game
Division of Sport Fish, Research and Technical Services
333 Raspberry Road, Anchorage, Alaska, 99518-1565

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*Nick A. DeCovich and Katherine G. Howard
Alaska Department of Fish and Game, Division of Commercial Fisheries,
333 Raspberry Road
Anchorage, AK, 99518USA*

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ABSTRACT

Significant genetic variation exists among populations of Chinook salmon (*Oncorhynchus tshawytscha*) within the Yukon River drainage, and has been used to provide estimates of the composition of mixed stock fishery harvests since the early 1990s. In 2009, a single nucleotide polymorphism (SNP) baseline was used to estimate the stock composition of Chinook salmon test fishery catches and harvests in the U.S. portion of the Yukon River. Of the samples collected from test, commercial, and subsistence fisheries, 3,361 individuals were assayed for genetic variation at 42 SNPs. Mixed stock analysis of these samples was used to estimate the stock composition of the harvest at 3 hierarchical levels: country of origin (U.S. and Canada), broad scale (Lower Yukon, Middle Yukon, and Canada), and fine scale (Lower Yukon, Upper U.S. Yukon, Tanana River, Canada Border, Pelly, Carmacks and Takhini). Inseason analyses provided important and timely information for fisheries managers, while additional postseason analyses provided a more thorough perspective of the stock composition of the run and harvests. In the Pilot Station test fishery, Canadian stocks contributed between 43% and 70% of the catch over 3 strata representing the main pulses of the run. In the subsistence fisheries, Canadian stocks contributed between 16% and 95% of the harvest.

Key words: Chinook salmon, *Oncorhynchus tshawytscha*, genetic stock identification, Yukon River, single nucleotide polymorphism, SNP, commercial fishery, subsistence

INTRODUCTION

Knowledge of the origin of Chinook salmon (*Oncorhynchus tshawytscha*) harvested in Yukon River fisheries is important for successful fisheries management. Under the Yukon River Salmon Agreement between the United States (U.S.) and Canada, U.S. fishery managers are obligated to pass a specified target range of Chinook salmon into Canada. This target range is comprised of an escapement goal and a harvest share of the total Canadian-origin run. Monitoring the proportion of Canadian-origin Chinook salmon in fishery harvests from U.S. waters of the Yukon River is critical for successfully meeting those obligations. Yukon River fisheries managers consider test fishery and commercial harvest numbers an important indicator of run size, and postseason genetic analyses have been very effective at distinguishing major stock components in the commercial catch since 2004. Previous studies on stock compositions of the commercial harvest in Districts Y-1 and Y-2 (Figure 1) have shown that the proportion of Canadian-origin fish may vary significantly within a season, with a contribution ranging from 25% to 69% of the harvest (Templin et al. 2006b; DeCovich and Templin 2009). Since 2004, the stock composition of Chinook salmon harvests in the subsistence and commercial Chinook salmon fisheries of the Yukon River has been estimated by genetic stock identification (GSI) techniques based on a comprehensive baseline of DNA markers (Beacham and Candy 2006; Templin et al. 2006a-b; Templin et al. 2008).

Two types of genetic markers have replaced the allozyme baseline developed in the 1990s (Beacham et al. 1989; Wilmot et al. 1992; Templin et al. 2005), single nucleotide polymorphisms (SNPs) (Smith et al. 2005a; Templin et al. 2006b) and microsatellites (Flannery et al. 2006; Templin et al. 2006a,c; Beacham et al. 2008). With the exception of microsatellite use in 2005, SNPs have been the preferred GSI technique for stock composition estimates of Yukon River Chinook salmon fisheries since 2004. A SNP is a single-base difference at a nucleotide position in a DNA sequence. The Human Genome Project and similar projects on other species have demonstrated that SNPs are ubiquitous throughout the genome. Since SNPs occur throughout the genome in many species, they are likely subject to a wider range of evolutionary rates than microsatellites, and are thus useful for addressing a broader range of questions (Brumfield et al. 2003; Morin et al. 2004). Because some SNPs are influenced by natural selection, they are particularly valuable for GSI applications where other markers cannot detect differences between

geographically close populations. For example, Miller et al. (2001) found that apparent differences in selection for SNPs in the major histocompatibility complex (MHC) locus indicated strong genetic distinction between nearby populations of sockeye salmon, in contrast to observations at neutral loci. Similarly, Beacham et al. (2001) demonstrated that SNPs involved in the immune system of salmon could provide as good or better resolution for genetic stock analyses than microsatellites.

This study describes the mixed stock analysis of the Chinook salmon test fishery catches and subsistence harvests in the U.S. portion of the Yukon River in 2009. We briefly describe the baseline used to analyze fishery samples, the simulations used to verify the accuracy and precision of estimated stock proportions, and report the results of the mixed stock analysis of fishery samples. The stock contribution estimates are provided for 3 hierarchical sets of reporting groups: 1) country of origin (U.S. and Canada), 2) broad scale (Lower Yukon, Middle Yukon, and Canada), and 3) fine scale (Lower Yukon, Tanana, Upper U.S. Yukon, Canada Border, Pelly, Carmacks and Takhini). Country of origin stock grouping is the primary focus of this study as it is most relevant to current fishery management needs.

OBJECTIVES

The goal of this project is to provide estimates of the stock composition of Chinook salmon catches in test fisheries, and harvests in commercial and subsistence fisheries on the Yukon River in 2009. Additionally, this is a pilot study to test the feasibility and application of inseason stock composition estimates from test fisheries in Chinook salmon fisheries management. The following objectives support the goals of this study:

- 1) Sample Chinook salmon from each commercial and subsistence fishery in districts Y-1 through Y-5 (Figure 1) as follows:
 - i. District Y-1 subsistence – 400 individuals
 - ii. District Y-1 commercial (collected from chum salmon-directed fishery) – 200 individuals per period
 - iii. District Y-2 commercial (collected from chum salmon-directed fishery) – 200 individuals per period
 - iv. District Y-3 subsistence – 250 individuals
 - v. District Y-4 subsistence – 250 individuals from each subdistrict
 - vi. District Y-5 commercial – 400 individuals
 - vii. District Y-5 subsistence – 400 individuals
- 2) Sample Chinook salmon throughout the duration of the Lower Yukon Test Fishery (LYTF) project – 600 individuals.
- 3) Sample Chinook salmon throughout the duration of the Pilot Station test fishery – 400 individuals.
- 4) Analyze a representative sample from each fishing district and period for genetic variation at the SNP loci in the baseline.
- 5) Estimate the relative contribution of stocks to the test, commercial, and subsistence fisheries of the Yukon River.
- 6) Analyze up to 5 groups of salmon from LYTF and Pilot Station projects, representing distinct pulses of fish. Provide inseason analyses to fishery managers within 36 hours of receipt of genetic tissues, for use in management decisions during the fishing season.

METHODS

BASELINE

A slightly modified version of the 25 population baseline described in Templin et al. (2008) was used for this analysis. The SNP baseline now consists of 27 populations and 52 SNPs. A subset of this baseline, consisting of all 27 populations and 42 SNPs, was used to provide the stock composition estimates reported in this study. The 42 SNPs used represent all polymorphic loci available for Yukon Chinook salmon populations. Additionally 2 populations were added to the baseline; the Chatanika River in the Tanana River drainage and a mainstem spawning population collected near Minto.

In the 2007 and 2008 version of the baseline, if linkage disequilibrium was significant in more than half of the collections, we produced composite phenotypes for each fish by combining the genotypes from these linked markers and treating them as a single locus in further analyses. Alternately, for 2009, we removed one locus from each pair of putatively linked loci.

Simulations were conducted to evaluate the accuracy and precision of the SNP baseline to provide compositional estimates of mixtures of Chinook salmon harvested in Yukon River fisheries. These simulations were used to help assess whether the baseline of allele frequencies at the 42 SNP markers would provide sufficient information to identify individual stocks or groups of stocks (reporting groups) in mixtures. Reporting groups for genetic stock identification of Yukon River Chinook salmon were defined in previous studies based on a combination of genetic similarity, geographic features, and management applications (Flannery et al. 2006).

Reporting groups were defined hierarchically into 3 levels: 1) country of origin, 2) broad scale, and 3) fine scale. The broad scale groups (Lower Yukon, Middle Yukon, and Canada) were the same regions previously used for estimating stock composition of the harvest by scale pattern analysis (JTC 1997). Simulations performed using fine-scale reporting groups represent identifiable sets of populations useful for management and research (Table 1) (Templin et al. 2006b).

Simulations were performed using the Statistical Package for Analyzing Mixtures (SPAM version 3.7, Debevec et al. 2000). Mixture genotypes were randomly generated from the baseline allele frequencies assuming Hardy-Weinberg equilibrium. Each simulated mixture ($N=400$) was composed entirely of the stock or reporting group under study. When a reporting group mixture was simulated, all stocks in the reporting group contributed equally to the mixture. Average estimates of mixture proportions and 90% confidence intervals were derived from 1,000 simulations. Reporting groups with mean correct estimates of 90% or better are considered highly identifiable in fishery applications (Seeb et al. 2000).

FISHERY COLLECTIONS

For all tissue sampling, axillary processes were collected and preserved in ethanol. Chinook salmon were sampled from the test, commercial, and subsistence fisheries in the U.S. portion of the river (Table 2; Figure 1). Samples were collected randomly during each fishing period (designated time when fishing is allowed) while sampling the harvest for age, sex, and length data (DuBois and DeCovich 2008). Test fishery sample collection occurred in the Coastal District (Dall Point), District Y-1 (LYTF) and District Y-2 (Pilot Station), and District Y-5 (Eagle sonar test fishery located near the U.S. /Canada border) (Table 2). Commercial harvest samples

were collected from Districts Y-1 and Y-2, and subsistence harvests were sampled in Districts Y-1, Y-3, Y-4, and Y-5 (Table 2). The subsistence samples from District Y-4 were collected from subdistricts Y-4A (Kaltag and Nulato), Y-4B (Bishop Rock and Galena), and Y-4C (Ruby). The subsistence samples from District Y-5 were collected from subdistricts Y-5C in the mainstem Yukon River above Hess Creek, at Rapids, and at Fort Yukon.

For LYTF and Pilot Station, an attempt was made to sample distinct pulses of Chinook salmon passing through the test fisheries, and analyze these samples inseason to support management objectives. LYTF samples were collected between June 1 and July 15, 2009 from all 3 mouths of the Yukon River, using set gillnets with 8.5-inch mesh. Pilot Station samples were collected from approximately June 9 through July 19, 2009, using a broad array of mesh size drift gillnets, ranging from 2.75-inch to 8.5-inch stretch mesh. Pulses were identified by increases in catch per unit effort (CPUE) for a sustained period of 3 to 5 days followed by a substantial decrease in CPUE. Samples were flown to the ADF&G Gene Conservation Laboratory (GCL) in Anchorage, analyzed and reported on within 36 hours of receipt at the GCL.

Commercial and subsistence fishery samples were analyzed postseason. Since samples from subdistrict Y-4A were collected from 2 locations, Kaltag and Nulato, and in subdistrict Y-4B from Bishop Mountain and Galena, stock composition estimates were calculated for these fisheries both by location (i.e., Kaltag and Nulato separately) and also by subdistrict (i.e., Kaltag and Nulato pooled). Samples from the Pilot Station Test Fishery and subdistrict Y-5C subsistence fishery at Rapids were also stratified temporally postseason. Sample sets were defined to be representative of catch proportion estimates while maintaining minimum sample size requirements.

LABORATORY METHODS

Genetic data were collected from the fishery samples as individual multi-locus genotypes for 42 SNPs (Table 3). The SNP data collected were individual diploid genotypes for each locus. More SNPs were assayed in this study than in 2008 (26 SNPs) because recent advancements in laboratory technology reduced the cost per genotype, and it is no longer cost effective for the GCL to run only 26 SNPs. Even though it would be most cost effective to assay 48 or 96 SNPs, only 42 SNPs have been found to be polymorphic in Yukon River Chinook salmon, and hence only 42 were used.

Genomic DNA was extracted using a DNeasy® 96 Tissue Kit by QIAGEN® (Valencia, CA).¹ Chinook salmon samples were genotyped using a BioMark 48.48 Dynamic Array (Fluidigm <http://www.fluidigm.com/products/biomark-genotype-profiling.html>), which systematically combines 48 samples and 48 assays into 2,304 parallel reactions. Each reaction was conducted in a 6.75 nL volume consisting of 1xTaqMan Universal Buffer (Applied Biosystems), 1.5 U AmpliTaq Gold DNA Polymerase (Applied Biosystems), 9 mM of each polymerase chain reaction (PCR) primer, 2 mM of each probe, 1xDA Assay Loading Buffer (Fluidigm), 12.5xROX (Invitrogen), and 0.01% Tween-20. Thermal cycling was performed on a BioMark IFC Cycler. The Dynamic Arrays were read on a BioMark Real-Time PCR System after amplification and scored using BioMark Genotyping Analysis software (Fluidigm).

¹ Product names used in this report are included for scientific completeness, but do not constitute a product endorsement.

QUALITY CONTROL METHODS

The following measures were implemented to ensure the quality and consistency of data produced by laboratory procedures:

- 1) Each individual was assigned a unique accession identifier. When DNA was extracted and analyzed from each individual, a sample sheet was created that linked each individual's code to a specific well in a uniquely numbered 96-well plate. This sample sheet accompanied the individual through all phases of a project, minimizing the risk of misidentification of samples.
- 2) Genotypes were assigned to individuals using a double-scoring system. Two researchers designated allele scores for each individual.
- 3) Approximately 8% of individuals, 8 samples from each 96-well DNA extraction plate, were reanalyzed for all SNPs. This provided a measure of reproducibility, discrepancy rates, and allowed for correction of any errors created during the processing of individual plates. Failure rates were calculated, representing the number of samples that did not amplify during PCR, averaged over all loci.
- 4) The final data were checked for duplicated multi-locus genotypes, an indication of errors caused prior to extraction of the DNA. When duplicate genotypes were found, the genotype was attributed to the first individual, and subsequent individuals with the same genotype were removed from the analysis.
- 5) The data have been permanently stored in an Oracle database, *LOKI*, administered by ADF&G.

MIXED STOCK ANALYSIS

Stock composition estimates for the stock groups of management interest were generated using BAYES (Pella and Masuda 2001). Individual population estimates were first calculated, and then summed into reporting regions (stocks). The estimation was run using a single chain, without thinning, and a Markov Chain Monte Carlo sample size of 10,000. Three chains were run beginning with different starting conditions. The Dirichlet prior distribution parameters for stock proportions were equal ($1/N$). Inference was founded on the posterior distribution based on a combined set of the last 5,000 steps of each chain. The mean of the posterior distribution is reported as the best estimate, and the central 90% of the distribution was reported as the 90% credibility interval.

Stock composition estimates were reported for 3 hierarchical levels when sample sizes were >200 as follows: 1) country of origin (U.S and Canada), 2) broad scale (Lower Yukon, Middle Yukon, and Canada), and 3) fine scale (Lower Yukon, Tanana, Upper U.S. Yukon, Canada Border, Pelly, Carmacks and Takhini). When sample sizes were <200 , only the first 2 levels of the hierarchy were reported. Increasing the resolution to 3 reporting groups in the U.S. (Lower River, Tanana, and Upper Koyukuk/Upper U.S. Yukon) has been supported by simulation studies of the baseline (Templin et al. 2006a). Primarily this study focuses on the country of origin reporting group, as this is most crucial for current fishery management objectives. The broad scale and fine scale estimates are given in the tables when sample sizes are sufficient.

RESULTS

COLLECTIONS

During 2009, 5,343 Chinook salmon were sampled as part of 13 collections from test, commercial, and subsistence fisheries in the U.S. portion of the Yukon River drainage (Table 2; Figure 1). Samples from Eagle sonar test fishery (Y-5) were shipped to the Canadian Department of Fisheries and Oceans (CDFO) genetics lab in Nanaimo B.C. for processing, but are included in Table 2 for completeness.

In 2009, all Yukon River commercial fishing targeted chum salmon, and only incidentally harvested Chinook salmon were sampled. Since the incidental sale of Chinook salmon was prohibited, only 11 fish were sampled in Y-1 and 10 in Y-2. Mesh sizes in this fishery were restricted to 6 inches or less for the purpose of targeting chum salmon. No samples from commercial harvests were analyzed in this study due to insufficient sample sizes. Likewise, samples from the Dall Point test fishery were too small to warrant analyses.

LABORATORY / QUALITY CONTROL ANALYSIS

Of the fishery samples, a total of 3,361 individuals were analyzed for allelic variation (Table 3). The quality control analysis demonstrated an overall discrepancy rate of 0.05%, which, if one assumes an equal error rate in the original and quality control genotyping process, represents an error rate of 0.03%. The overall genotyping failure rate was 2.25%, and ranged from a low of 0.70% for samples collected at Kaltag to a high of 4.66% for samples collected from the LYTF at Big Eddy.

BASELINE ANALYSIS

Linkage disequilibrium within each collection yielded significant results in >90% of collections at 2 marker pairs: *Ots_FGF6A* and *Ots_FGF6B*; and *Ots_HSP90B-100* and *Ots_HSP90B-385*. The second marker in each pair, *Ots_FGF6B* and *Ots_HSP90B-385*, was removed from subsequent analyses.

Simulations

All fine scale reporting regions had mean correct allocations of >90% for the 100% simulation tests. Only 3 reporting regions, Upper U.S., Stewart, and Carmacks had lower 90% confidence interval bounds of less than 90% (0.856, 0.868, and 0.885, respectively) (Table 4).

MIXED STOCK ANALYSIS

Test Fishery

Fishing conditions in the LYTF made it difficult to detect specific pulses of Chinook salmon. Therefore, the decision was made to shift some of the inseason analysis efforts to the Pilot Station test fishery for the purpose of characterizing the stock composition of the run.

The first pulse of Chinook salmon was identified by the LYTF and 296 samples collected from June 3 through June 17 (south mouth) and June 18 (north and middle mouths) were flown to the GCL and analyzed (Figure 2). Stock composition estimates indicated that the proportion of Canadian-origin Chinook salmon present in the first pulse at LYTF was 63% for the south mouth (Big Eddy) (Table 5), and 53% for north and middle mouths (Middle Mouth) (Table 6). Sample

sizes could not support fine scale analyses for this pulse, though broad scale analyses from the south mouth samples revealed that the majority of the U.S.-origin fish were bound for the Middle Yukon (Table 5).

For the second pulse at LYTF, 204 samples were caught between June 18 and June 22, flown to the GCL and analyzed (Figure 2). Stock composition estimates indicated that the proportion of Canadian-origin Chinook salmon present in the LYTF for this time period was 63% for the south mouth (Big Eddy) (Table 5) and 45% for north and middle mouths (Middle Mouth) (Table 6). Again, samples sizes were not sufficient to support fine scale analyses and broad scale analyses of south mouth samples indicated that most U.S.-origin fish in this pulse originated in the Middle Yukon.

First pulse samples from the Pilot Station test fishery caught through June 15 were also flown to the GCL and analyzed concurrently with the samples from the first pulse at the LYTF. In general, sampling at Pilot Station was conducted in proportion to the passage estimate determined by the sonar project (Figure 3). Stock composition estimates indicated that the proportion of Canadian-origin Chinook salmon present in Pilot Station test fishery for this time period was 70%, with the majority of US-bound fish originating in the Middle Yukon (Table 7; Figure 4).

An additional 2 inseason analyses were completed for the Pilot Station test fishery. Pulses were difficult to detect in this fishery, and samples were flown back to the GCL based on the availability of a U.S. Fish and Wildlife Service (USFWS) aircraft making scheduled flights between Pilot Station and Anchorage. The strata used for these inseason analyses are shown in Figure 3 and represent the samples caught between June 9-15 (Stratum 1), June 16-24 (Stratum 2) and June 26-29 (Stratum 3). Stock composition estimates indicated that the proportion of Canadian-origin Chinook salmon present in the Pilot Station test fishery for these strata ranged from 70% in Stratum 1 to 43% in Stratum 3 (Table 7; Figure 4). Only Stratum 2 had sufficient sample size to warrant fine scale analyses, and Carmacks-origin Chinook salmon were the most prevalent small scale stock grouping within that time period (Table 7).

Postseason, after reviewing the complete daily sonar passage estimates and all available genetic samples, new strata were constructed for Pilot Station test fishery samples (Figure 5). Once the additional samples were assayed, stock composition estimates were re-calculated for the new strata. The Canadian-origin Chinook salmon present in the Pilot Station test fishery ranged from a high of 68% in Stratum 1 to a low of 17% in Stratum 4, and there was a distinct shift towards lower river stocks during the progression of the run (Table 8; Figure 6).

Commercial

No samples from commercial fisheries were analyzed due to insufficient sample sizes.

Subsistence

In the District Y-1 subsistence fishery, 63% of the harvest samples were comprised of Canadian populations (Table 9). The Pelly region was the largest contributor to the Canadian component at 22%. Of the U.S. contribution, the largest component was estimated to be from the Lower Yukon (25%), while populations from the Tanana River contributed 23% of the harvest. The harvest from the Y-3 subsistence fishery showed a lower proportion of Canadian populations (26%), while the Lower Yukon component was larger than in District Y-1 (51%) (Table 10).

The estimated contribution of Canadian populations to the subsistence harvest in District Y-4 varied from a high of 59% in Kaltag (subdistrict Y-4A) to a low of 16% in Ruby (subdistrict Y-4C) (Tables 11–13; Figure 7). The Carmacks region comprised the greatest portion of the Canadian estimate in subdistricts Y-4A and Y-4B (there were insufficient samples for fine-scale analysis of subdistrict Y-4C).

Samples were collected at Rapids throughout the run. Out of 701 samples collected, 411 samples representing 2 pulses were analyzed. The Canadian contribution to the subsistence harvest in subdistrict Y-5C, was 95% for both the first stratum at Rapids (June 21–July 1) and Fort Yukon, with the dominant fine scale reporting group being Canadian Border and Carmacks, respectively. The Canadian contribution to the second stratum at Rapids (July 16–July 31) was 82%. The Canadian contribution to the subsistence sample harvested from the mainstem Yukon River above Hess Creek was 70% (Table 14).

DISCUSSION

The 2009 Yukon River Chinook salmon run abundance was below average, and projections indicated that Chinook salmon abundance would not support normal subsistence harvests in Alaska (approximately 50,000 Chinook salmon), meet escapement goals in Alaska, and meet the interim management escapement goal (IMEG) of >45,000 Canadian-origin fish. Because of the particular concern for Canadian-origin stocks in recent years, GSI information was an important indicator for inseason management. Despite low overall run strength estimated at Pilot Station sonar early in the run, inseason GSI information on the Canada-bound proportion of the run identified a stronger presence of these stocks than had been documented during 2007 and 2008.

Because of the low run strength estimated at Pilot Station sonar, unprecedented management actions were implemented on subsistence fisheries and there was no commercial fishery for Chinook salmon. Delays in subsistence fishing activity, due to management actions, resulted in subsistence harvests with different genetic compositions than those observed in recent years.

Also confounding GSI analyses, high water conditions and debris early in the season made sampling the first part of the run difficult at the LYTF and Pilot Station test fisheries, and early arriving fish were likely missed at both locations. Ice dams moving down the river caused substantial flooding along an extensive portion of the Yukon River. This flooding coincided with the start of the Chinook salmon run. Once it was determined that pulses would be undetectable in the LYTF, efforts were shifted to analyzing catches from the Pilot Station test fishery. The proposed objective of sampling 3 pulses of Chinook salmon passing through the LYTF was not achieved.

Postseason examination of daily fish passage at Pilot Station sonar revealed that the initial inseason strata could be modified to create 4 new strata with the fourth stratum represented by all available samples through the end of the season. These strata were intended to represent the 4 quartiles of the run passing through the Pilot Station test fishery. The major difference between the inseason and postseason estimates is the dramatic increase in Lower Yukon stocks in the fourth stratum. This result was expected based on previous years' GSI studies showing the bulk of the Canadian-origin component of the run to pass through the lower river by the midpoint of the run (Templin et al. 2006b; Templin et al. 2008; DeCovich and Templin 2009).

While the country of origin reporting group has been the focus of this study, the patterns seen in fine scale reporting group estimates are generally similar to past years. For example, in the Pilot

Station test fishery, the Pelly region makes up the highest proportion of the Canadian component in the early time strata, and the Carmacks region predominates in later time strata. This is a pattern seen in previous years in both Pilot Station samples (DeCovich et. al 2010), and in Lower Yukon River fishery harvests (Templin et. al. 2008). Lower Yukon River stocks are generally present in low proportions in earlier time strata, and dominate the stock composition in later time strata. This pattern is seen in test fishery catches, and in harvests from commercial and subsistence fisheries (DeCovich et. al 2010; Templin et. al. 2008).

Improvements to the baseline could improve overall estimates, particularly for fine scale reporting groups. The baseline used for this analysis has been proven, through simulation studies, to provide accurate and precise stock composition estimates at each level of the hierarchy. However, not all spawning populations are present in the baseline. Gaps in baseline population coverage are present in the Koyukuk, Tanana, and Porcupine drainages. Also, several spawning populations from rivers in U.S. waters near the U.S./Canada border are absent from the baseline. The ADF&G Anadromous Waters Catalog lists the Kandik, Nation, and Tatonduk rivers as having spawning populations of Chinook salmon (Johnson and Blanche 2010). The absence of these populations in the baseline could bias the results of mixed-stock analysis if individuals from these populations are present in mixture samples. For example, if these populations are genetically more similar to those in Canadian waters, individuals from these populations would be allocated to the Canadian component under our current model. This bias will be small if these border rivers support relatively small populations of Chinook salmon. However, further study is warranted to assess the size of these populations, characterize their genetic stock structure, and evaluate any implications to mixed-stock analysis models.

Postseason analyses could also be enhanced with more strategic subsistence sampling efforts, to identify and then better capture particular harvest patterns in some communities. For instance, in 2009, sampling efforts in Y-4 were expanded to include the subsistence fishery located along the mainstem Yukon River near Hess Creek, which had not been characterized in previous years. Additionally, the community of Ruby appears to have harvest patterns that are not representative of the rest of its district. In 2009, the Canadian proportion was 16% in the sample from Ruby, and the Middle Yukon component was 78%. This is similar to the results of the 2007 analysis, where the Tanana component dominated the Ruby sample. It is hypothesized that since the bulk of the fish sampled at Ruby come from the south bank, Chinook salmon caught at this location are following the plume of water generated by the Tanana River. Unfortunately, the 2009 sample size from Ruby was not large enough to estimate the fine-scale stock groupings. Future studies should attempt to attain a larger sample size from Ruby, so that the Tanana component, which is included in the Middle Yukon group, could be estimated.

As has been seen in previous years, GSI analyses demonstrate a pattern of generally increasing harvest of Canadian-origin Chinook salmon in upper fishing districts. As the farthest upstream fishing subdistrict, Y-5C subsistence fishery samples were predominately Canadian-origin fish. Within Y-5C, the lowest Canadian component (70%) was estimated from the mainstem sample near Hess Creek. This seems reasonable since this sample is the furthest downstream sample of the entire subdistrict Y-5C samples, thus increasing the potential that U.S. populations could be present in the harvest.

Despite the tremendous challenges of sampling and providing timely information inseason, GSI analyses provided important insight for fisheries managers to make timely decisions during the 2009 fishing season. Yukon River managers will continue to use this information, in conjunction

with run abundance indices, to make stock-specific management decisions. Because each season presents a unique set of challenges, the utility of inseason analyses will continue to be evaluated in subsequent seasons. Postseason analyses have been useful to managers to understand harvest patterns among various regions of the Yukon River and to better understand potential impacts of different management actions. In light of the recent volatility of Canadian-origin stocks, GSI analysis has proven necessary, and improvements to the genetic baseline and sampling strategies will only improve the power of this technique for fisheries management on the Yukon River.

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TABLES AND FIGURES

Table 1.–Chinook salmon collections from the Yukon River drainage organized hierarchically into reporting groups for mixed stock analysis using genetic stock identification.

Country	Broad scale	Fine scale	Population	Year(s)	Sample size
United States					
	Lower Yukon				
		Lower Yukon			
			Andrafsky River	2003	208
			Anvik River	2002	99
			Tozitna River	2002, 2003	450
			Gisasa River	2001	228
	Middle Yukon				
		Upper U.S. Yukon			
			Sheenjek River	2002, 2004, 2006	51
			Beaver Creek	1997	100
			Chandalar River	2002, 2003, 2004	178
			Henshaw Creek	2001	150
			S. Fork Koyukuk River	2003	56
		Tanana River			
			Kantishna River	2005	200
			Chatanika River	2001, 2007	50
			Chena River	2001	200
			Salcha River	2005	200
Canada					
	Canada				
		Border			
			Chandindu River	2001	158
			Klondike River	2001, 2003	80
		Pelly			
			Mayo River	1997, 2003	62
			Stewart River	1997	99
			Blind Creek	1997, 2003	139
			Pelly River	1996, 1997	150
		Carmacks			
			Little Salmon	1987, 1997	100
			Big Salmon	1987, 1997	119
			Mainstem at Minto	2007	105
			Tatchun Creek	1987, 1997, 2002, 2003	169
			Nordenskiold River	2003	56
			Nisutlin River	1987, 1997	56
		Takhini			
			Takhini River	1997, 2003	101
			Whitehorse Hatchery	1985, 1987, 1997	242
				Total	3,651

Table 2.–Chinook salmon collections from test fishery catches, and commercial and subsistence fishery harvests in the Yukon River drainage, 2009.

District	Gear Type	Location	Target	Sample size	Number Analyzed
Commercial					
Y-1	≤6 Restricted	Emmonak	1,000	11	0
Y-2	≤6 Restricted	Saint Marys	800	10	0
Total Commercial			1,800	21	0
Subsistence					
Y-1	SGN	Emmonak	400	174	174
Y-3	SGN	Holy Cross	250	133	133
Y-4A	DGN	Kaltag	250	205	205
Y-4A	SGN	Nulato	250	386	386
Y-4B	SGN	Bishop Rock	250	191	191
Y-4B	SGN/ DGN	Galena	250	315	315
Y-4C	SGN/ FW	Ruby	250	144	144
Total Y-4 Subsistence			1,250	1,241	1,241
Y-5B	FW	Tanana-north bank	300	0	
Y-5C	Unknown	Mainstem- near Hess Creek	0	190	190
Y-5C	FW	Rapids	900	701	411
Y-5C	SGN/FW	Fort Yukon	250	151	151
Total Y-5 Subsistence			1,450	1,042	752
Total Subsistence			2,700	2,283	1,993
Test Fishery					
Y-1	DGN	Dall Point	600	3	0
Y-1	SGN	LYTF-Big Eddy	600	511	300
	SGN	LYTF-Big Eddy (mesh study)	800	480	0
Y-1	SGN	LYTF-Middle Mouth	600	529	200
Total LYTF			2,000	1,520	500
Y-2	DGN	Pilot Station	600	868	868
	DGN	Eagle Sonar	500	648	0
Total Test Fishery			3,700	3,039	1,368
Grand Total			8,200	5,343	3,361

Note: Gear types used were set gillnet (SGN), drift gillnet (DGN), and fish wheels (FW). Commercial fisheries in Districts Y-1 and Y-2 used drift gillnets with ≤6 inch restricted mesh sizes.

Table 3.–Single nucleotide polymorphisms assayed in individual Chinook salmon sampled in the U.S. portion of the Yukon River drainage, 2009.

Locus	Source
<i>GTH2B-550</i>	GAPs locus
<i>NOD1</i>	GAPs locus
<i>Ots_E2-275</i>	Smith et al. 2005a
<i>Ots_arf-188</i>	Smith et al. 2005a
<i>Ots_AsnRS-60</i>	Smith et al. 2005a
<i>E9BAC</i>	GAPs locus
<i>Ots_ETIF1A</i>	GAPs locus
<i>Ots_FARSLA-220</i>	Smith et al. 2007
<i>Ots_FGF6A</i>	Unpublished
<i>Ots_GH2</i>	Smith et al. 2005b
<i>Ots_GPDH-338</i>	Smith et al. 2005a
<i>Ots_GPH-318</i>	Smith et al. 2007
<i>Ots_GST-207</i>	Smith et al. 2007
<i>Ots_hmRNPL-533</i>	Smith et al. 2007
<i>Ots_HSP90B-100</i>	Smith et al. 2007
<i>Ots_IGF-I.1-76</i>	Smith et al. 2005a
<i>Ots_Ikaros-250</i>	Smith et al. 2005a
<i>Ots_il-1racp-166</i>	Smith et al. 2005a
<i>Ots_LEI-292</i>	Smith et al. 2007
<i>Ots_MHC1</i>	Smith et al. 2005b
<i>Ots_MHC2</i>	Smith et al. 2005b
<i>Ots_ZNF330-181</i>	Smith et al. 2005a
<i>Ots_LWSop-638</i>	Smith et al. 2005a
<i>Ots_SWS1op-182</i>	Smith et al. 2005a
<i>Ots_P450</i>	Smith et al. 2005b
<i>Ots_P53</i>	Smith et al. 2005b
<i>Ots_Prl2</i>	Smith et al. 2005b
<i>Ots_ins-115</i>	Smith et al. 2005a
<i>Ots_SClkF2R2-135</i>	Smith et al. 2005a
<i>Ots_SERPC1-209</i>	Smith et al. 2007
<i>Ots_SL</i>	Smith et al. 2005b
<i>Ots_TAPBP</i>	GAPs locus
<i>Ots_Tnsf</i>	Smith et al. 2005b
<i>Ots_u202-161</i>	Smith et al. 2005a
<i>Ots_u211-85</i>	Smith et al. 2005a
<i>Ots_U212-158</i>	Smith et al. 2005a
<i>Ots_u4-92</i>	Smith et al. 2005a
<i>Ots_u6-75</i>	Smith et al. 2005a
<i>Ots_Zp3b-215</i>	Smith et al. 2005a
<i>RAG3</i>	GAPs locus
<i>S7-1</i>	GAPs locus
<i>unkn526</i>	GAPs locus

Table 4.–Mean reporting group allocations of simulated mixtures of Yukon River Chinook salmon from the baseline of 26 SNPs.

Reporting Region		Est	90% CI
Country			
	United States	0.983	(0.962-0.999)
	Canada	0.987	(0.965-1.000)
Broad-scale			
	Lower Yukon	0.990	(0.975-1.000)
	Middle Yukon	0.971	(0.941-0.994)
	Canada	0.987	(0.965-1.000)
Fine-scale			
	Lower Yukon	0.988	(0.969-0.999)
	Upper US	0.921	(0.856-0.973)
	Tanana	0.951	(0.905-0.991)
	Canada Border	0.973	(0.946-0.995)
	Stewart	0.929	(0.868-0.988)
	Carmacks	0.943	(0.885-0.987)
	Takhini	0.973	(0.936-0.997)

Table 5.–Estimated proportional contributions (Est), standard deviations (SD), and 90% credibility intervals by reporting group of Chinook salmon caught in the Lower Yukon Test Fishery, Big Eddy site, from stratum 1 and 2 in 2009.

Reporting Group	Stratum 1			Stratum 2			
	June 5-17			June 18-22			
	<i>N</i> =	Est	90% CI	<i>N</i> =	Est	90% CI	
Country							
	United States	0.375	0.048	(0.298-0.455)	0.368	0.07	(0.255-0.487)
	Canada	0.625	0.048	(0.545-0.702)	0.632	0.07	(0.513-0.745)
Broad-scale							
	Lower Yukon	0.074	0.024	(0.037-0.117)	0.104	0.037	(0.051-0.170)
	Middle Yukon	0.301	0.047	(0.225-0.380)	0.265	0.068	(0.157-0.381)
	Canada	0.625	0.048	(0.545-0.702)	0.632	0.07	(0.513-0.745)

Note: The estimated reporting group proportions are given for each of 3 hierarchical levels. Samples sizes (*N*) allowed for country of origin and broad scale estimates only.

Table 6.–Estimated proportional contributions (Est), standard deviations (SD), and 90% credibility intervals by reporting group of Chinook salmon caught in the Lower Yukon Test Fishery, Middle Mouth site, from stratum 1 and 2 in 2009.

Reporting Group	Stratum 1			Stratum 2		
	June 5-18			June 18-22		
	<i>N</i> = Est	100 SD	90% CI	<i>N</i> = Est	100 SD	90% CI
Country						
United States	0.474	0.069	(0.362-0.589)	0.549	0.062	(0.447-0.650)
Canada	0.526	0.069	(0.411-0.638)	0.451	0.062	(0.350-0.553)

Note: The estimated reporting group proportions are given for each of 3 hierarchical levels. Samples sizes (*N*) allowed for country of origin estimates only.

Table 7.—Estimated proportional contributions (Est), standard deviations (SD), and 90% credibility intervals by reporting group of Chinook salmon caught in the Pilot Station test fishery, as analyzed inseason, from stratum 1, 2, and 3 in 2009.

Reporting Group	Stratum 1			Stratum 2			Stratum 3		
	June 9-15			June 16-24			June 26-29		
	N= Est	121 SD	90% CI	N= Est	441 SD	90% CI	N= Est	159 SD	90% CI
Country									
United States	0.297	0.051	(0.217-0.384)	0.53	0.036	(0.470-0.590)	0.57	0.05	(0.488-0.651)
Canada	0.703	0.051	(0.616-0.783)	0.47	0.036	(0.410-0.530)	0.43	0.05	(0.349-0.512)
Broad-scale									
Lower Yukon	0.047	0.032	(0.000-0.106)	0.165	0.024	(0.127-0.207)	0.366	0.049	(0.286-0.448)
Middle Yukon	0.25	0.054	(0.165-0.342)	0.364	0.038	(0.302-0.427)	0.204	0.048	(0.129-0.286)
Canada	0.703	0.051	(0.616-0.783)	0.47	0.036	(0.410-0.530)	0.43	0.05	(0.349-0.512)
Fine-scale									
Lower Yukon				0.165	0.024	(0.127-0.207)			
Upper U.S. Yukon				0.163	0.054	(0.082-0.256)			
Tanana				0.202	0.045	(0.123-0.273)			
Canada Border				0.046	0.027	(0.000-0.092)			
Pelly				0.168	0.048	(0.093-0.250)			
Carmacks				0.245	0.041	(0.178-0.312)			
Takhini				0.012	0.014	(0.000-0.039)			

Note: The estimated reporting group proportions are given for each of 3 hierarchical levels. The estimated group proportions are given for each of 3 hierarchical levels.

Table 8.—Estimated proportional contributions (Est), standard deviations (SD), and 90% credibility intervals by reporting group of Chinook salmon caught in the Pilot Station test fishery, as analyzed postseason, from stratum 1, 2, 3, and 4 in 2009.

Reporting Group	Stratum 1			Stratum 2			Stratum 3			Stratum 4		
	June 9-16			June 17-22			June 23-29			June 30 - July 19		
	N=	SD	90% CI	N=	SD	90% CI	N=	SD	90% CI	N=	SD	90% CI
Country												
United States	0.321	0.051	(0.241-0.408)	0.473	0.04	(0.408-0.539)	0.589	0.042	(0.519-0.658)	0.828	0.036	(0.767-0.883)
Canada	0.679	0.051	(0.592-0.759)	0.527	0.04	(0.461-0.592)	0.411	0.042	(0.342-0.481)	0.172	0.036	(0.117-0.233)
Broad-scale												
Lower Yukon	0.038	0.027	(0.000-0.088)	0.153	0.027	(0.111-0.200)	0.288	0.036	(0.229-0.348)	0.691	0.043	(0.620-0.759)
Middle Yukon	0.283	0.053	(0.199-0.374)	0.32	0.04	(0.255-0.388)	0.301	0.043	(0.231-0.373)	0.137	0.035	(0.082-0.199)
Canada	0.679	0.051	(0.592-0.759)	0.527	0.04	(0.461-0.592)	0.411	0.042	(0.342-0.481)	0.172	0.036	(0.117-0.233)
Fine-scale												
Lower Yukon				0.153	0.027	(0.111-0.200)	0.288	0.036	(0.229-0.348)			
Upper U.S. Yukon				0.094	0.048	(0.015-0.177)	0.144	0.052	(0.065-0.234)			
Tanana				0.226	0.045	(0.152-0.299)	0.157	0.046	(0.084-0.233)			
Canada Border				0.074	0.031	(0.027-0.127)	0.025	0.02	(0.000-0.062)			
Pelly				0.232	0.056	(0.140-0.326)	0.105	0.059	(0.003-0.204)			
Carmacks				0.213	0.045	(0.144-0.291)	0.258	0.049	(0.179-0.340)			
Takhini				0.008	0.012	(0.000-0.033)	0.023	0.021	(0.000-0.062)			

Note: The estimated reporting group proportions are given for each of 3 hierarchical levels.

Table 9.—Estimated proportional contributions (Est), standard deviations (SD), 90% credibility intervals (CI), and analyzed sample size (*N*) of Chinook salmon harvested in the District Y-1 subsistence fishery, 2009.

Y-1 Subsistence				
Reporting Group		<i>N</i> = Est	174 SD	90% CI
Country				
	United States	0.637	0.049	(0.555-0.716)
	Canada	0.363	0.049	(0.284-0.445)
Broad-scale				
	Lower Yukon	0.249	0.045	(0.177-0.325)
	Middle Yukon	0.387	0.053	(0.302-0.477)
	Canada	0.363	0.049	(0.284-0.445)
Fine-scale				
	Lower Yukon	0.249	0.045	(0.177-0.325)
	Upper U.S. Yukon	0.158	0.054	(0.076-0.253)
	Tanana	0.229	0.054	(0.143-0.321)
	Canada Border	0.070	0.028	(0.029-0.120)
	Pelly	0.226	0.060	(0.129-0.327)
	Carmacks	0.064	0.045	(0.000-0.143)
	Takhini	0.003	0.007	(0.000-0.018)

Note: The estimated group proportions are given for each of 3 hierarchical levels when possible.

Table 10.—Estimated proportional contributions (Est), standard deviations (SD), 90% credibility intervals (CI), and analyzed sample size (*N*) of Chinook salmon harvested in the District Y-3 subsistence fishery, 2009.

Y-3 Holy Cross				
Reporting Group		<i>N</i> =	238	
		Est	SD	90% CI
Country				
	United States	0.743	0.035	(0.684-0.798)
	Canada	0.257	0.035	(0.202-0.316)
Broad-scale				
	Lower Yukon	0.515	0.036	(0.456-0.575)
	Middle Yukon	0.227	0.037	(0.169-0.289)
	Canada	0.257	0.035	(0.202-0.316)
Fine-scale				
	Lower Yukon	0.515	0.036	(0.456-0.575)
	Upper U.S. Yukon	0.119	0.034	(0.067-0.178)
	Tanana	0.108	0.029	(0.064-0.158)
	Canada Border	0.008	0.015	(0.000-0.043)
	Pelly	0.032	0.038	(0.000-0.110)
	Carmacks	0.217	0.042	(0.146-0.284)
	Takhini	0.001	0.003	(0.000-0.005)

Note: The estimated group proportions are given for each of 3 hierarchical levels when possible.

Table 11.—Estimated proportional contributions (Est), standard deviations (SD), 90% credibility intervals (CI), and analyzed sample size (*N*) of Chinook salmon harvested in the District Y-4A subsistence fisheries, 2009.

Y-4A Kaltag				Y-4A Nulato		
Reporting Group	<i>N</i> = Est	204 SD	90% CI	<i>N</i> = Est	384 SD	90% CI
Country						
United States	0.419	0.044	(0.348-0.491)	0.530	0.035	(0.473-0.587)
Canada	0.581	0.044	(0.509-0.652)	0.470	0.035	(0.413-0.527)
Broad-scale						
Lower Yukon	0.069	0.034	(0.017-0.128)	0.104	0.025	(0.064-0.147)
Middle Yukon	0.350	0.050	(0.270-0.434)	0.426	0.038	(0.364-0.489)
Canada	0.581	0.044	(0.509-0.652)	0.470	0.035	(0.413-0.527)
Fine-scale						
Lower Yukon	0.069	0.034	(0.017-0.128)	0.104	0.025	(0.064-0.147)
Upper U.S. Yukon	0.147	0.050	(0.067-0.233)	0.138	0.041	(0.074-0.209)
Tanana	0.203	0.050	(0.123-0.286)	0.288	0.044	(0.215-0.360)
Canada Border	0.002	0.007	(0.000-0.013)	0.020	0.019	(0.000-0.056)
Pelly	0.190	0.056	(0.099-0.284)	0.119	0.047	(0.042-0.196)
Carmacks	0.379	0.056	(0.290-0.474)	0.314	0.048	(0.235-0.392)
Takhini	0.010	0.017	(0.000-0.047)	0.017	0.017	(0.000-0.049)

Note: The estimated group proportions are given for each of 3 hierarchical levels when possible.

Table 12.—Estimated proportional contributions (Est), standard deviations (SD), 90% credibility intervals (CI), and analyzed sample size (*N*) of Chinook salmon harvested in the District Y-4B subsistence fisheries, 2009.

Y-4B Bishop Mountain				Y-4B Galena		
Reporting Group	<i>N</i> = Est	191 SD	90% CI	<i>N</i> = Est	311 SD	90% CI
Country						
United States	0.612	0.048	(0.531-0.691)	0.637	0.038	(0.573-0.699)
Canada	0.388	0.048	(0.309-0.469)	0.363	0.038	(0.301-0.427)
Broad-scale						
Lower Yukon	0.131	0.034	(0.081-0.190)	0.106	0.027	(0.064-0.153)
Middle Yukon	0.480	0.055	(0.389-0.569)	0.531	0.043	(0.461-0.600)
Canada	0.388	0.048	(0.309-0.469)	0.363	0.038	(0.301-0.427)
Fine-scale						
Lower Yukon				0.106	0.027	(0.064-0.153)
Upper U.S. Yukon				0.181	0.061	(0.080-0.279)
Tanana				0.350	0.055	(0.261-0.442)
Canada Border				0.043	0.021	(0.006-0.080)
Pelly				0.135	0.042	(0.066-0.205)
Carmacks				0.184	0.038	(0.125-0.249)
Takhini				0.001	0.004	(0.000-0.008)

Note: The estimated group proportions are given for each of 3 hierarchical levels when possible.

Table 13.—Estimated proportional contributions (Est), standard deviations (SD), 90% credibility intervals (CI), and analyzed sample size (*N*) of Chinook salmon harvested in the District Y-4C subsistence fishery, 2009.

Y-4C Ruby				
Reporting Group		<i>N</i> =	144	
		Est	SD	90% CI
Country				
	United States	0.841	0.037	(0.778-0.899)
	Canada	0.159	0.037	(0.101-0.222)
Broad-scale				
	Lower Yukon	0.060	0.028	(0.020-0.112)
	Middle Yukon	0.781	0.044	(0.706-0.851)
	Canada	0.159	0.037	(0.101-0.222)
Fine-scale				
	Lower Yukon			
	Upper U.S. Yukon			
	Tanana			
	Canada Border			
	Pelly			
	Carmacks			
	Takhini			

Insufficient Samples

Note: The estimated group proportions are given for each of 3 hierarchical levels when possible.

Table 14.—Estimated proportional contributions (Est), standard deviations (SD), 90% credibility (CI), and analyzed sample size (N) of Chinook salmon harvested in the District Y-5C subsistence fisheries, 2009.

Y-5C Mainstem (above Hess)			Y-5C Rapids			Stratum 2			Y-5C Fort Yukon			
			Stratum 1			Stratum 2						
			June 21 - July 1			July 16 - July 31						
Reporting Group	N =	189		N =	295		N =	116		N =	151	
	Est	SD	90% CI	Est	SD	90% CI	Est	SD	90% CI	Est	SD	90% CI
Country												
United States	0.302	0.058	(0.208-0.399)	0.047	0.034	(0.002-0.109)	0.183	0.053	(0.102-0.273)	0.051	0.037	(0.005-0.122)
Canada	0.698	0.058	(0.601-0.792)	0.953	0.034	(0.891-0.998)	0.817	0.053	(0.727-0.898)	0.949	0.037	(0.878-0.995)
Broad-scale												
Lower Yukon	0.004	0.007	(0.000-0.018)	0.002	0.004	(0.000-0.009)	0.023	0.021	(0.000-0.064)	0.003	0.007	(0.000-0.015)
Middle Yukon	0.299	0.059	(0.204-0.397)	0.046	0.034	(0.001-0.107)	0.160	0.053	(0.079-0.252)	0.048	0.037	(0.002-0.120)
Canada	0.698	0.058	(0.601-0.792)	0.953	0.034	(0.891-0.998)	0.817	0.053	(0.727-0.898)	0.949	0.037	(0.878-0.995)
Fine-scale												
Lower Yukon				0.002	0.004	(0.000-0.009)				0.003	0.007	(0.000-0.015)
Upper U.S. Yukon				0.042	0.035	(0.000-0.104)				0.033	0.038	(0.000-0.110)
Tanana				0.004	0.008	(0.000-0.023)				0.015	0.019	(0.000-0.054)
Canada Border	<i>Insufficient Samples</i>			0.467	0.044	(0.395-0.538)	<i>Insufficient Samples</i>			0.127	0.044	(0.058-0.203)
Pelly				0.431	0.053	(0.342-0.518)				0.358	0.083	(0.224-0.495)
Carmacks				0.055	0.031	(0.005-0.111)				0.385	0.080	(0.257-0.518)
Takhini				0.000	0.002	(0.000-0.003)				0.079	0.038	(0.016-0.145)

Note: The estimated group proportions are given for each of 3 hierarchical levels when possible.

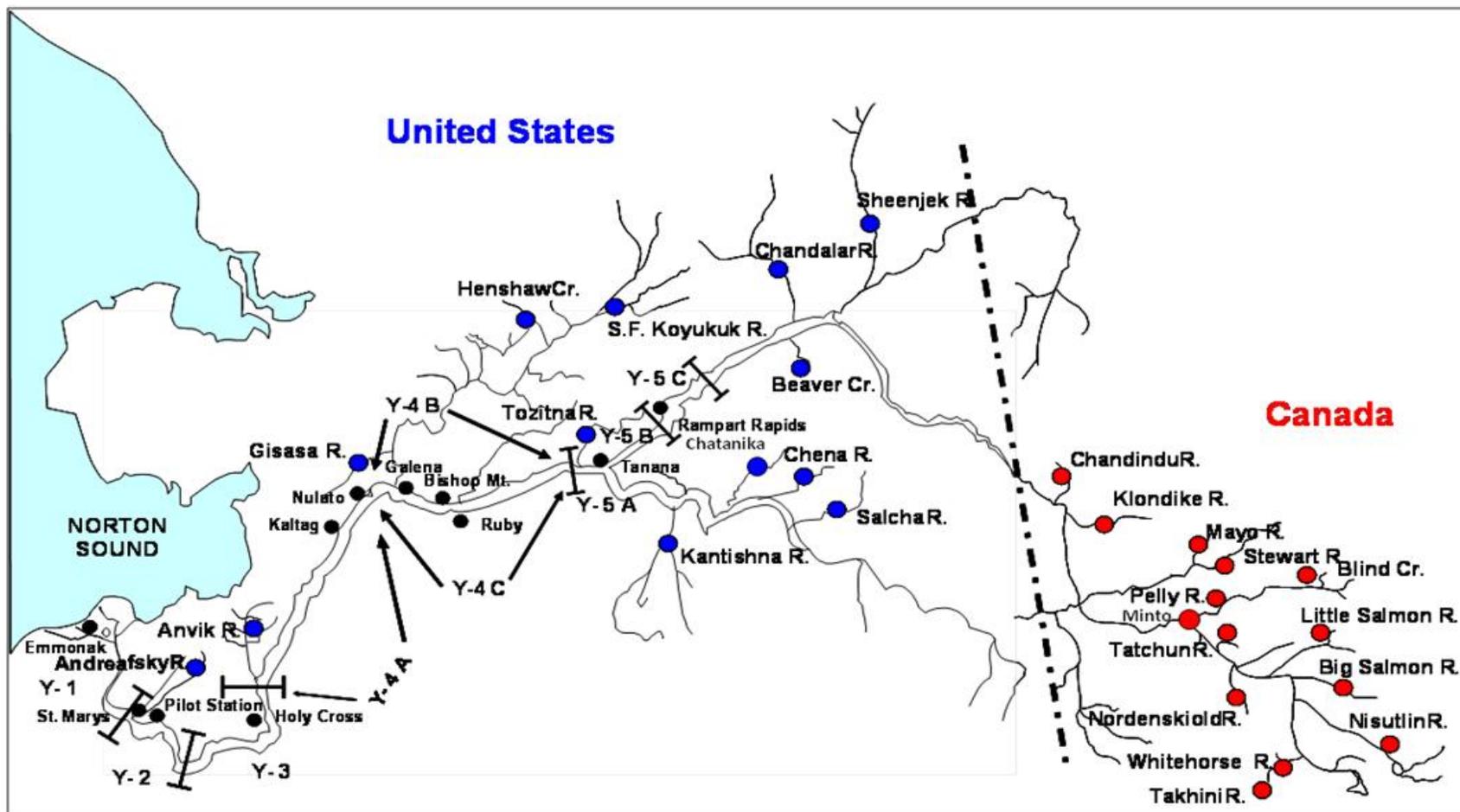
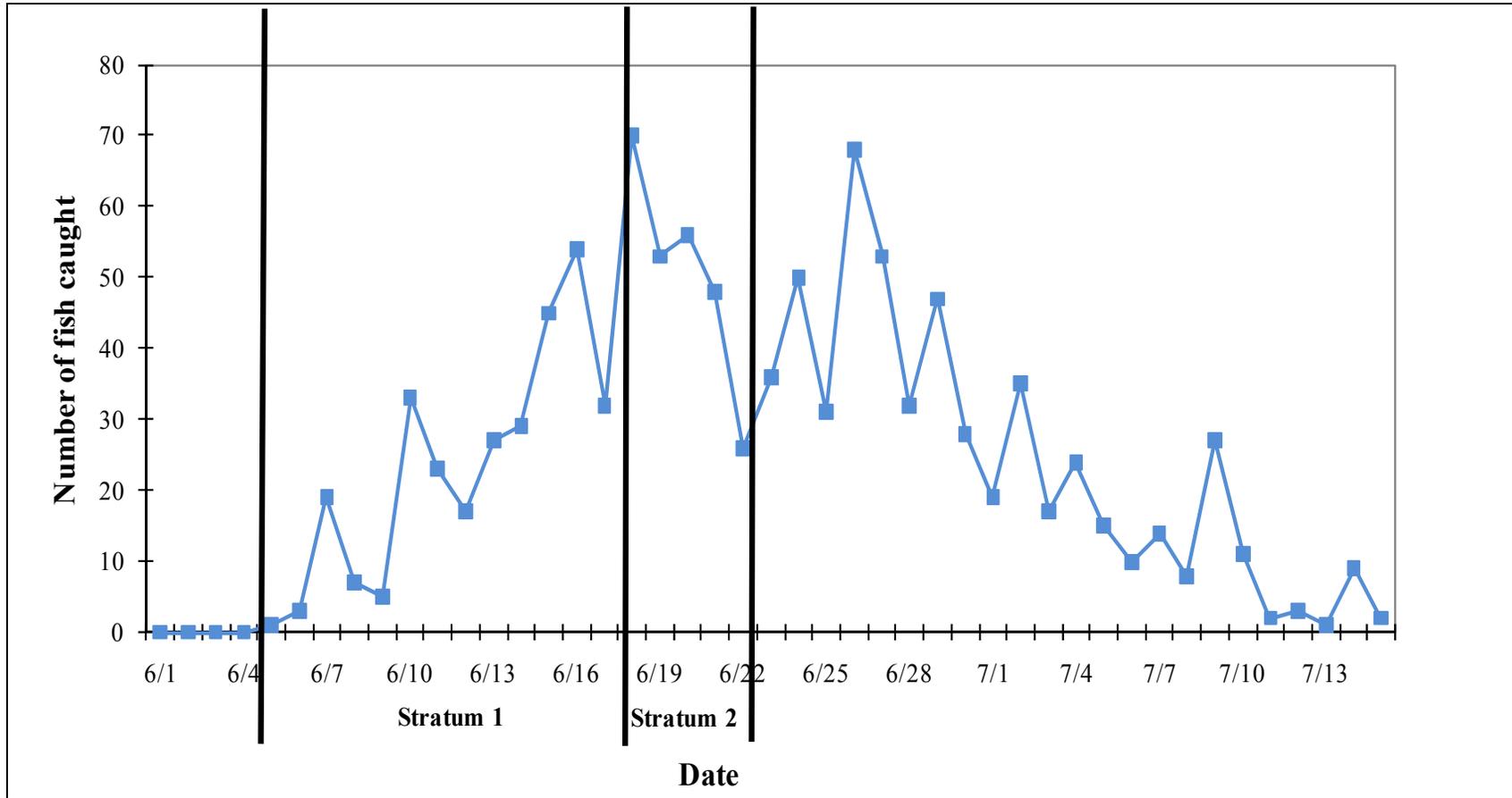
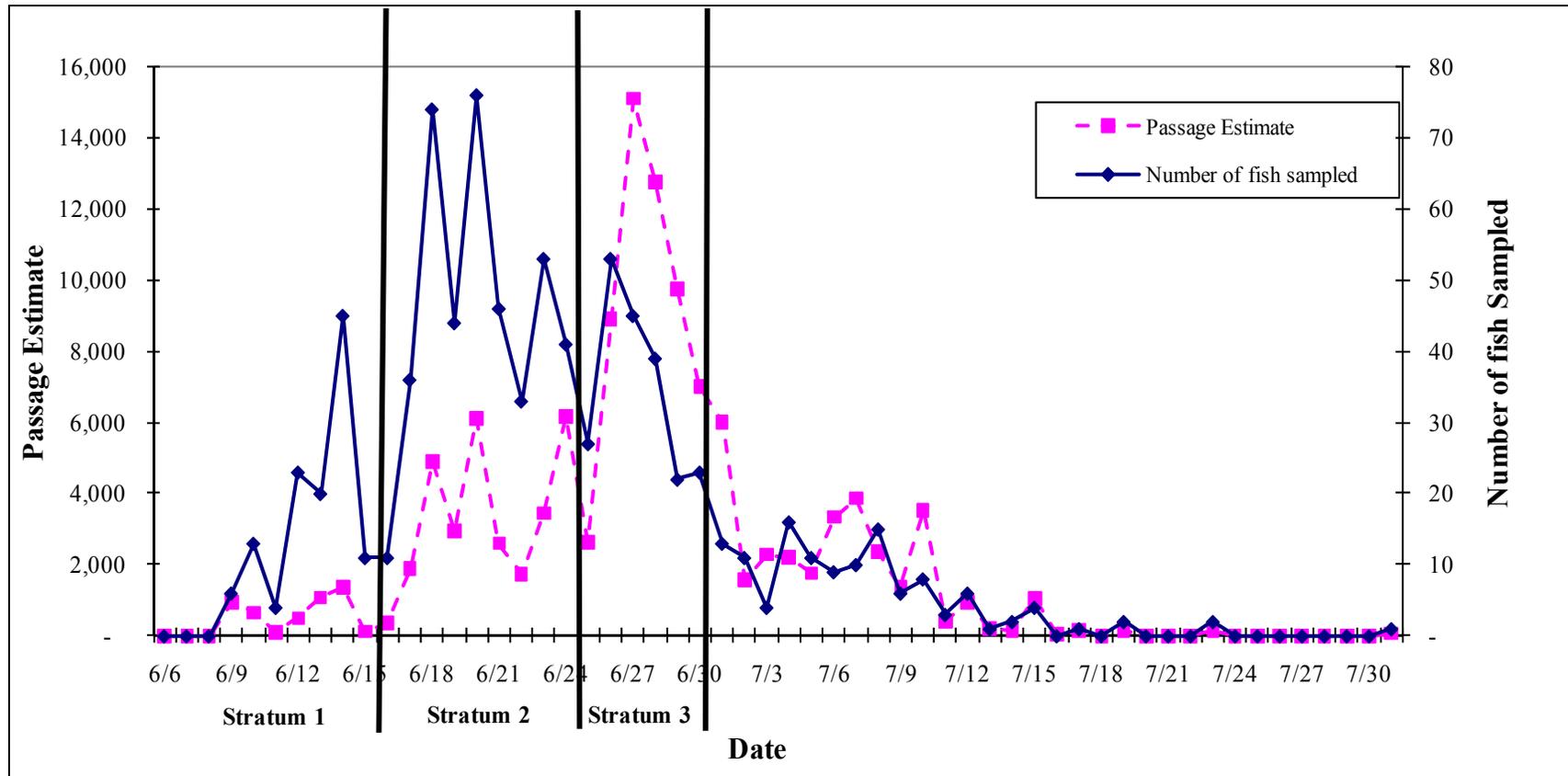


Figure 1.—Baseline collection locations, and fishing districts (and mainstem subdistricts) used for management of salmon fisheries in the United States portion of the Yukon River drainage.



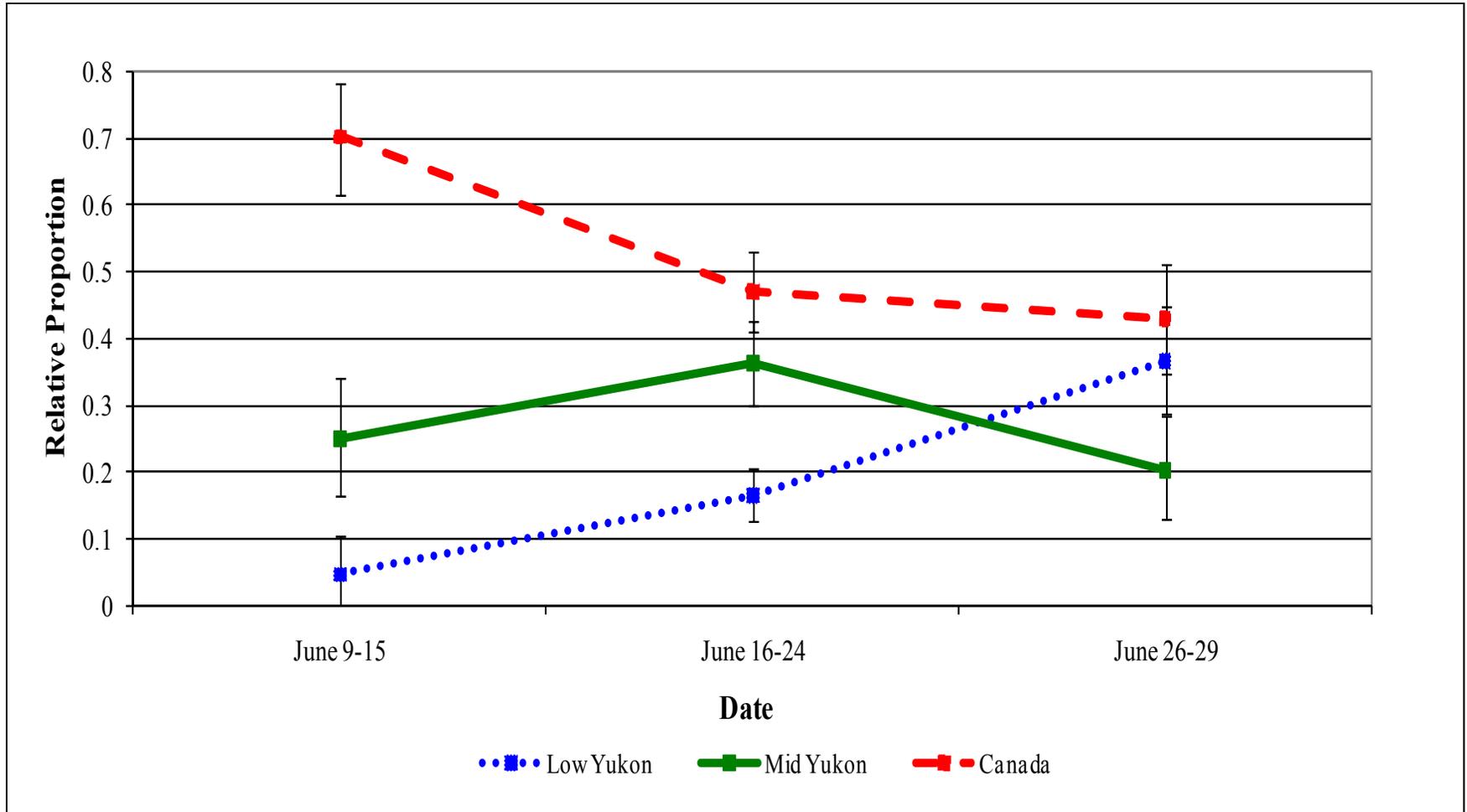
Note: Vertical lines denote the temporal separation of collections for creating strata for GSI estimates.

Figure 2.—Daily catch of Chinook salmon in the LYTF, 2009.



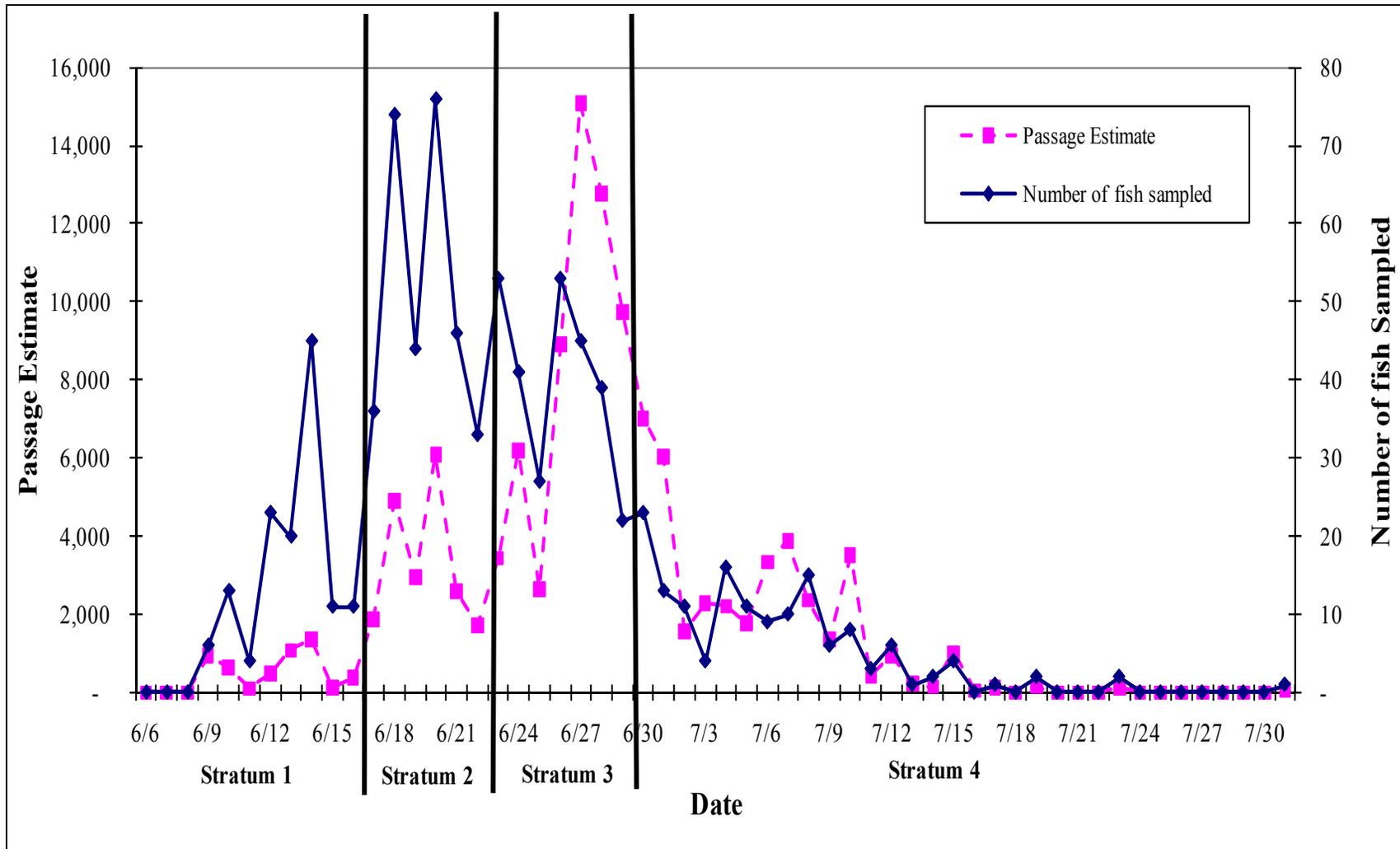
Note: Vertical lines denote the temporal separation of collections for creating inseason strata for GSI estimates.

Figure 3.—Daily sample size of Chinook salmon from the Pilot Station test fishery and daily passage estimates, 2009.



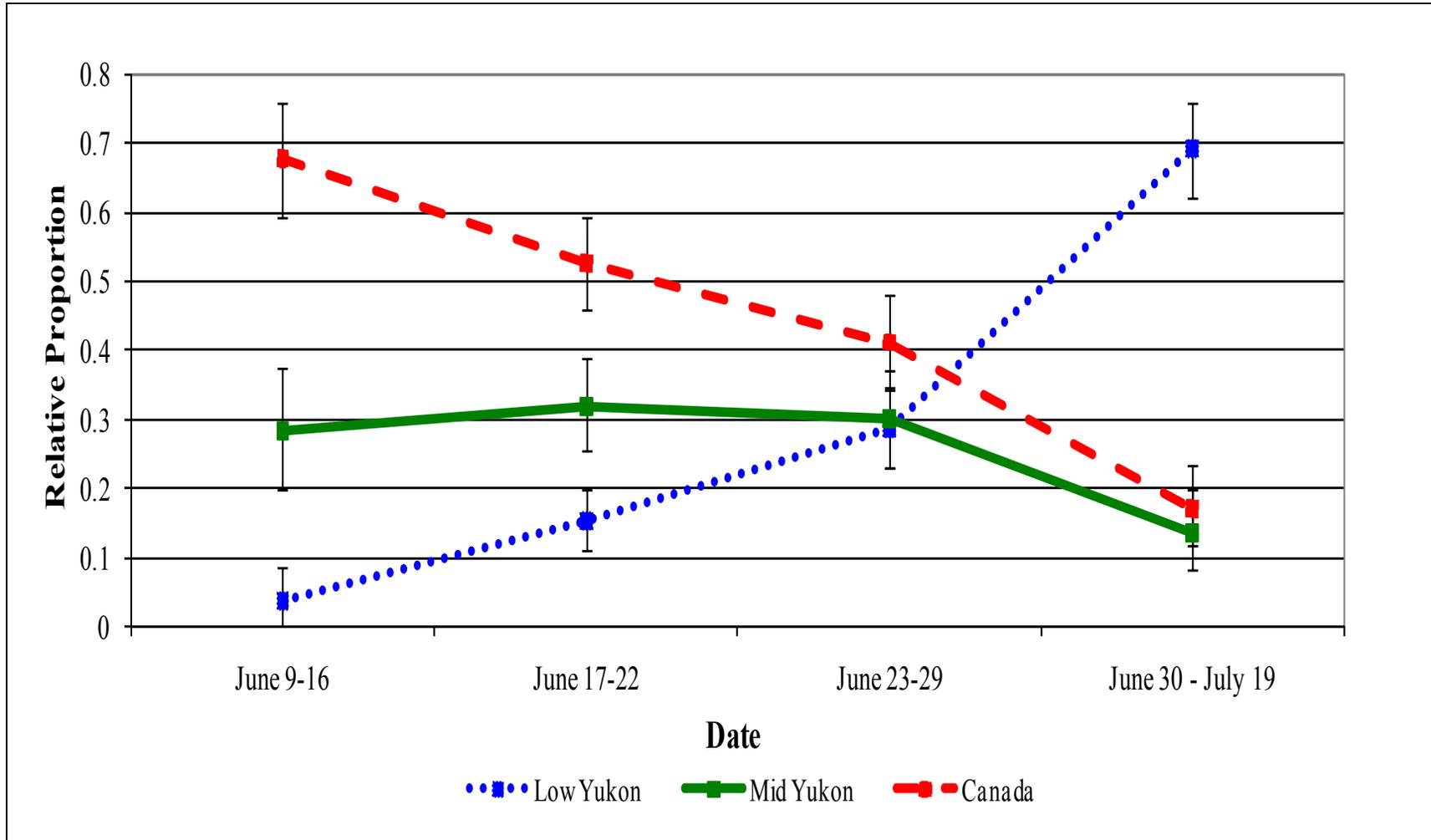
Note: Error bars denote the bounds of the 90% credibility interval.

Figure 4.—Relative stock composition of 3 broad-scale reporting groups in the Chinook salmon caught in the Pilot Station Test Fishery, as analyzed inseason, 2009.



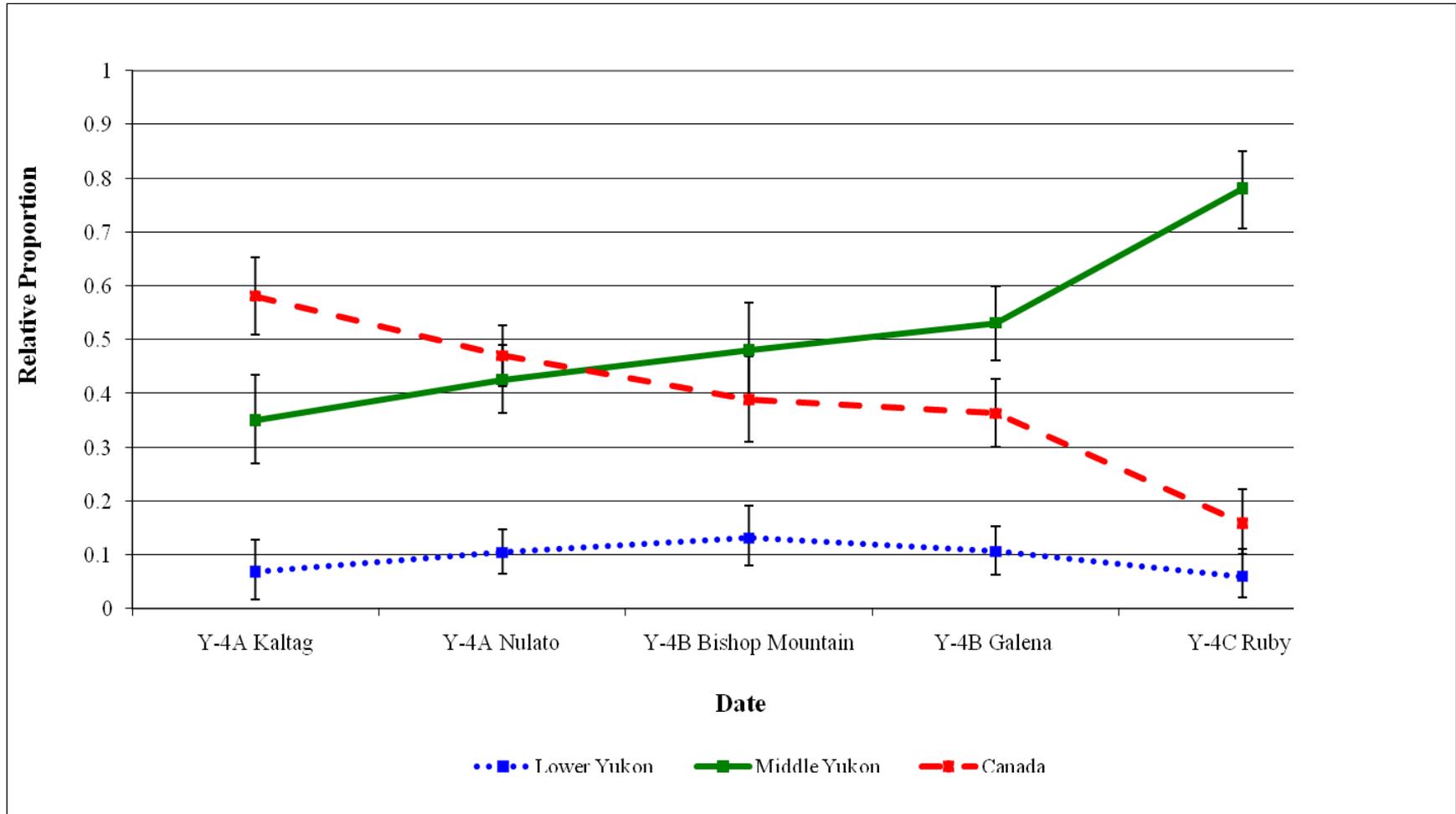
Note: Vertical lines denote the temporal separation of collections for creating postseason strata.

Figure 5.—Daily sample size of Chinook salmon from the Pilot Station test fishery and daily passage estimates, 2009.



Note: Error bars denote the bounds of the 90% credibility interval.

Figure 6.—Relative stock composition of 3 broad-scale reporting groups in the Chinook salmon caught in the Pilot Station Test Fishery, as analyzed postseason, 2009.



Note: Error bars denote the bounds of the 90% credibility interval.

Figure 7.—Relative stock composition of 3 broad-scale reporting groups in the Chinook salmon caught in District Y-4 subsistence fisheries, 2009.